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SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
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<120> GAMMA PGA CONJUGATES FOR ELICITING IMMUNE RESPONSES DIRECTED
AGAINST BACILLI

<130> 4239-68226-07

<150> PCT/US2004/017736
<151> 2004-06-04

<150> US 60/476,598
<151> 2003-06-05

<160> 3

<170> PatentIn version 3.2

<210> 1
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<213> Artificial Sequence

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<223> Basic peptide derived from HIV-1 Tat protein.

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tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa 96
Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys

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cag gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Gln Gly Leu 35 40 45			144
cta gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val 50 55 60			192
acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu 65 70 75 80			240
aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly 85 90 95			288
ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct Phe Ile Lys Val Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala 100 105 110			336
gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys 115 120 125			384
gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln 130 135 140			432
ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp 145 150 155 160			480
ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser 165 170 175			528
agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser 180 185 190			576
aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp 195 200 205			624
aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp 210 215 220			672
gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His 225 230 235 240			720
gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser 245 250 255			768
acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att			816

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Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile			
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gat aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat			
Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr			864
275	280	285	
ccg att gta cat gta gat atg gag aat att att ctc tca aaa aat gag			
Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu			912
290	295	300	
gat caa tcc aca cag aat act gat agt caa acg aga aca ata agt aaa			
Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys			960
305	310	315	320
aat act tct aca agt agg aca cat act agt gaa gta cat gga aat gca			
Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala			1008
325	330	335	
gaa gtg cat gcg tcg ttc ttt gat att ggt ggg agt gta tct gca gga			
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cta gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct			
Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala			1152
370	375	380	
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Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr			1200
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gct cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa			
Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys			1248
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Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln			1296
420	425	430	
ata ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc			
Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile			1344
435	440	445	
gca tta aat gca caa gac gat ttc agt tct act cca att aca atg aat			
Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn			1392
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tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat			
Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp			1440
465	470	475	480
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Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly			1488
485	490	495	

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ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta gaa Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu	530	535 540
acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca ttt Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe	545	550 555 560
gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile	565	570 575
acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys	580	585 590
aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta gat Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp	595	600 605
aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg	610	615 620
ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val	625	630 635 640
gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu	645	650 655
ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat att Leu Leu Asn Ile Asp Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile	660	665 670
gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg	675	680 685
tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe	690	695 700
ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn	705	710 715 720
ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile	725	730 735
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		2016
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Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
740 745 750

att tta atc ttt tct aaa aaa ggc tat gag ata gga taa 2295
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755 760

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<213> Bacillus anthracis

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Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
50 55 60

Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
65 70 75 80

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
85 90 95

Phe Ile Lys Val Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
100 105 110

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
115 120 125

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
130 135 140

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
145 150 155 160

Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
165 170 175

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Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
180 185 190

Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
195 200 205

Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
210 215 220

Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
225 230 235 240

Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
245 250 255

Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
260 265 270

Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
275 280 285

Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
290 295 300

Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
305 310 315 320

Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
325 330 335

Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
340 345 350

Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys

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Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln		
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Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile		
435	440	445
Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn		
450	455	460
Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp		
465	470	475
480		
Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly		
485	490	495
Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln		
500	505	510
Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn		
515	520	525
Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu		
530	535	540
Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe		
545	550	555
560		
Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile		
565	570	575
Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys		
580	585	590
Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp		
595	600	605
Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg		
610	615	620
Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val		
625	630	635
640		

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Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
755 760